

Interactive Visualization of Biological Databases Using Information-Rich Virtual Environments

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Computational modeling and databasing of biological phenomena provide significant benefits for basic or applied biomedical research, as well as education. A major objective is to produce integrated information-rich biological databases that capture the complexity of reality and facilitate new discovery. (Such databases may contain experimental or simulated data or both.) Such databases may be characterized as integrating diverse data types including: *spatial* representations of physical phenomena, spanning multiple levels of organization from anatomical to cellular to molecular, *temporal* data for time series tracking of movement or concentration, and *abstract* data such as functional genomics/proteomics experimental data, functional annotations for sequences, or biochemical reactions. In order to derive maximum value from information-rich databases, effective user interfaces and visualizations that facilitate *insight generation* are absolutely critical. Maximum value will be achieved from these databases when biomedical scientists are able to explore and navigate them in multiple ways, relating effects between spatial, temporal, abstract, and other data types. Most current virtual environments and information visualizations lack the usability and support for such complex information-rich databases.

PathSim (*PATH*Hogen *SIM*ulation) is an example of a modeling strategy that makes extensive use of complex databases for both input and output. The main goal of *PathSim* is to model a variety of viral agents infecting a human host, from first exposure to viral clearance. The *PathSim* interface allows an end-user to explore anatomy, physiology, and, ultimately, cellular biochemistry. We are constructing and evaluating **information-rich virtual environments** (IRVEs) as part of the *PathSim* project. These IRVEs may also be applied to other similar information-rich databases in the life sciences that share the characteristics described above.

An IRVE combines the capabilities of *virtual environments* and *information visualization* to support integrated exploration of both spatial and embedded abstract data. Biologists will view the simulated physical structures of the model in a 3D virtual environment, interact with visually embedded abstract data, navigate across levels of biological hierarchy, *e.g.*, organs, tissues, cells, choose data for display, and manage simulation runs all within an integrated environment. For example, a user might decide to examine the effect of titer on the course of infection. Within the IRVE, the user deposits virions in the locations to be infected. After the simulation commences, the user revisits the IRVE to view signaling events initiated by virus deposition at the molecular level. Later, the user examines how fast the virus is spreading, killing cells, or recruiting immune cells to the vicinity. All activities are viewable in the virtual environment, with interactive links and data export to a suite of analytic tools. The IRVE operates on a wide range of hardware, from standard desktop displays to high-performance immersive CAVEs (CAVE Automatic Virtual Environment).